

1 GTCGACCCACGCGTCCGCAGCCTTCTCAGTATGGACCAAAGTACCCAAGCCTGTGCTGGT 60
 1 M D Q S T Q A C A G 10
 61 GAGAAACATTGCCATAACAGGGGTGGCCTACACTTCAGAATGCTTCCCCTGCAAACCTGG 120
 11 E K H C H N R G G L H F R M L P L Q T W 30
 121 CACGTATGCAGACAAGCAGGGCTCCTCTTTCTGCAAACCTTGCCCAGCAACTCTTATTCA 180
 31 H V C R Q A G L L F L Q T L P S N S Y S 50
 181 AATAAAGGAGAACTTCTTGCCACCAGTGTGACCCTGACAAATACTCAGAGAAAGGATCT 240
 51 N K G E T S C H Q C D P D K Y S E K G S 70
 241 TCTTCCTGTAACGTGCGCCCAGCTTGCACAGACAAAGATTATTTCTACACACACACGGCC 300
 71 ~~S S C~~ N V R P A C T D K D Y F Y T H T A 90
 301 TGCGATGCCAACGGAGAGACACAACCTCATGTACAAATGGGCCAAGCCGAAAATCTGTAGC 360
 91 C D A N G E T Q L M Y K W A K P K I C S 110
 361 GAGGACCTTGAGGGGGCAGTGAAGCTGCCTGCCTCTGGTGTGAAGACCCACTGCCCACCC 420
 111 E D L E G A V K L P A S G V K T H C P P 130
 421 TGCAACCCAGGCTTCTTCAAAACCAACAACAGCACCTGCCAGCCCTGCCCATATGGTTCC 480
 131 C N P G F F K T N N S T C Q P C P Y G S 150
 481 TACTCCAATGGCTCAGACTGTACCCGCTGCCCTGCAGGGACTGAACCTGCTGTGGGATTT 540
 151 Y S N G S D C T R C P A G T E P A V G F 170
 541 GAATACAAATGGTGAACACGCTGCCCACAAACATGGAACGACCGTTCTCAGTGGGATC 600
 171 E Y K W W N T L P T N M E T T V L S G I 190
 601 AACTTCGAGTACAAGGGCATGACAGGCTGGGAGCTGGCTGCTGATCACATTTACACAGCT 660

FIG.1A

191 N F E Y K G M T G W E V A G D H I Y T A 210

661 GCTGGAGCCTCAGACAATGACTTCATGATTCTCACTCTGGTTGTGCCAGGATTAGACCT 720

211 A ~~G A S D N D~~ F M I L T L V V P G F R P 230

721 CCGCAGTCGGTGATGGCAGACACAGAGAATAAAGAGCTGGCCAGAATCACATTGTCTTT 780

231 P Q S V M A D T E N K E V A R I T F V F 250

781 GAGACCCTCTGTTCTGTGAAGTGTGAGCTCTACTTCATGGTGGGTGTGAATTCTAGGACC 840

251 E T L C S V N C E L Y F M V G V N S R T 270

841 AACACTCCTGTGGAGACGTGGAAAGGTCCAAAGGCAAACAGTCCTATACCTACATCATT 900

271 N T P V E T W K G S K G K Q S Y T Y I I 290

901 GAGGAGAACACTACCACGAGCTTCACCTGGGCCTTCCAGAGGACCACTTTTCATGAGGCA 960

291 E E N T T T S F T W A F Q R T T F H E A 310

961 AGCAGGAAGTACACCAATGACCTTGCCAAGATCTACTCCATCAATGTCACCAATGTTATG 1020

311 S R K Y T N D V A K I Y S I N V T N V M 330

1021 AATGGCGTGGCCTCCTACTGCCGTCCCTGTGCCCTAGAAGCCTCTGATGTGGGCTCCTCC 1080

331 N G V A S Y C R P C A L E A S D V G S S 350

1081 TGCACCTCTTGTCTGCTGGTTACTATATTGACCGAGATTCAGGAACCTGCCACTCCTGC 1140

351 C T S C P A G Y Y I D R D S G T C H S C 370

1141 CCCCCTAACACAATTCTGAAAGCCCACCAGCCTTATGGTGTCCAGGCCTGTGTGCCCTGT 1200

371 P P N T I L K A H Q P Y G V Q A C V P C 390

1201 GGTCCAGGGACCAAGAACAACAAGATCCACTCTCTGTGCTACAATGATTGCACCTTCTCA 1260

391 G P G T K N N K I H S L C Y N D C T F S 410

FIG.1B

1261 CGCAACTCCAACCAGGACTTTCAACTACAACCTCTCCGCTTTGGCAAACACCGTCACT 1320
 411 R N T P T R T F N Y N F S A L A N T V T 430

1321 CTTGCTGGAGGGCCAAGCTTCACTTCCAAAGGGTTGAAATACTTCCATCACTTTACCCTC 1380
 431 L A G G P S F T S K G L K Y F H H F T L 450

1381 AGTCTCTGTGGAAACCAGGGTAGGAAAATGTCTGTGTGCACCGACAATGTCACTGACCTC 1440
 451 S L C G N Q G R K M S V C T D N V T D L 470

1441 CGGATTCCCTGAGGGTGAGTCAGGGTTCTCCAAATCTATCACAGCCTACGTCTGCCAGGCA 1500
 471 R I P E G E S G F S K S I T A Y V C Q A 490

1501 GTCATCATCCCCCAGAGGTGACAGGCTACAAGCCGGGGTTTCCTCACAGCCTGTCAGC 1560
 491 V I I P P E V T G Y K A G V S S Q P V S 510

1561 CTTGCTGATCGACTTATTGGGGTGACAACAGATATGACTCTGGATGGAATCACCTCCCCA 1620
 511 L A D R L I G V T T D M T L D G I T S P 530

1621 GCTGAACTTTTCCACCTGGAGTCCTTGGGAATACCGGACGTGATCTTCTTTTATAGGTCC 1680
 531 A E L F H L E S L G I P D V I F F Y R S 550

1681 AATGATGTGACCCAGTCCTGCAGTTCTGGGAGATCAACCACCATCCGCGTCAGGTGCAGT 1740
 551 N D V T Q S C S S G R S T T I R V R C S 570

1741 CCACAGAAACTGTCCCTGGAAGTTTGCTGCTGCCAGGAACGTGCTCAGATGGGACCTGT 1800
 571 P Q K T V P G S L L L P G T C S D G T C 590

1801 GATGGCTGCAACTTCCACTTCCTGTGGGAGAGCGCGGCTGCTTGCCCGCTCTGCTCAGTG 1860
 591 D G C N F H F L W E S A A A C P L C S V 610

1861 GCTGACTACCATGCTATCGTCAGCAGCTGTGTGGCTGGGATCCAGAAGACTACTTACGTG 1920

FIG.1C

611 A D Y H A I V S S C V A ~~G I Q K T~~ T Y V 630

1921 TGGCGAGAACCCAAGCTATGCTCTGGTGGCATTCTCTGCCTGAGCAGAGAGTCACCATC 1980

631 W R E P K L C S G G I S L P E Q R V T I 650

1981 TGCAAAACCATAGATTCTGGCTGAAAGTGGGCATCTCTGCAGGCACCTGTACTGCCATC 2040

651 C K T I D F W L K V ~~G I S A G T C T A I~~ 670

2041 CTGCTCACCGTCTTGACCTGCTACTTTTGGAAAAAGAATCAAAACTAGAGTACAAGTAC 2100

671 L L T V L T C Y F W K K N Q K L E Y K Y 690

2101 TCCAAGCTGGTGATGAATGCTACTCTCAAGGACTGTGACCTGCCAGCAGCTGACAGCTGC 2160

691 S K L V M N A T L K D C D L P A A D S C 710

2161 GCCATCATGGAAGGCGAGGATGTAGAGGACGACCTCATCTTTACCAGCAAGAATCACTCT 2220

711 A I M E G E D V E D D L I F T S K N H S 730

2221 TTGGGAAGATCAAATCATTTACCTCCAAGAGGACTCCTGATGGATTGACTCAGTGCCGC 2280

731 L G R S N H L P P R G L L M D L T Q C R 750

2281 TGAAGACATCCTCAGGAGGCCAGACATGGACCTGTGAGAGGCACTGCCTGCCTCACCTG 2340

751 * 751

2341 CCTCCTCACCTGCATAGCACCTTTGCAAGCCTGCGGCGATTTGGGTGCCAGCATCCTGC 2400

2401 AACACCCACTGCTGGAAATCTCTTCATTGTGGCCTTATCAGATGTTTGAATTCAGATCT 2460

2461 TTTTTTATAGAGTACCCAAACCCTCCTTTCTGCTTGCCTCAAACCTGCCAAATATACCCA 2520

2521 CACTTTGTTGTAAATTAAAAAAAAAAAAAAAAAAAA 2554

FIG.1D

		10	20	30	
1	M D O S T Q A C A G E K H C H N R G G L H F R M L P L Q T W	TR13.aa			
1	M - - - - - C V G A R R - L G R G P - - - - -	gi 472958 OX40 homologue			
		40	50	60	
31	H V C R O A G L L F L O T L P S N S Y S N K G E T S C H O C	TR13.aa			
13	- - C - - A A L L L L - G L G L S T V T G - - - - - L H C	gi 472958 OX40 homologue			
		70	80	90	
61	D P D K Y S E K G S S S C N V R P A C T D K D Y F Y T H T A	TR13.aa			
32	V G D T Y P S N D R C C H E C R P G - - - - -	gi 472958 OX40 homologue			
		100	110	120	
91	C D A N G E T Q L M Y K W A K P K I C S E D L E G A V K L P	TR13.aa			
50	- - - - - N G M V S R C	gi 472958 OX40 homologue			
		130	140	150	
121	A S G V K T H C P P C N P G F F K T N N S T C Q P C P Y G S	TR13.aa			
57	S R S Q N T V C R P C G P G F Y N - D V V S S K P C - - - -	gi 472958 OX40 homologue			
		160	170	180	
151	Y S N G S D C T R C P A G T E P A V G F E Y K W W N T L P T	TR13.aa			
82	- - - - K P C T W C - - - - -	gi 472958 OX40 homologue			
		190	200	210	
181	N M E T T V L S G I N F E Y K G M T G W E V A G D H I Y T A	TR13.aa			
88	- - - - -	gi 472958 OX40 homologue			

FIG. 2A

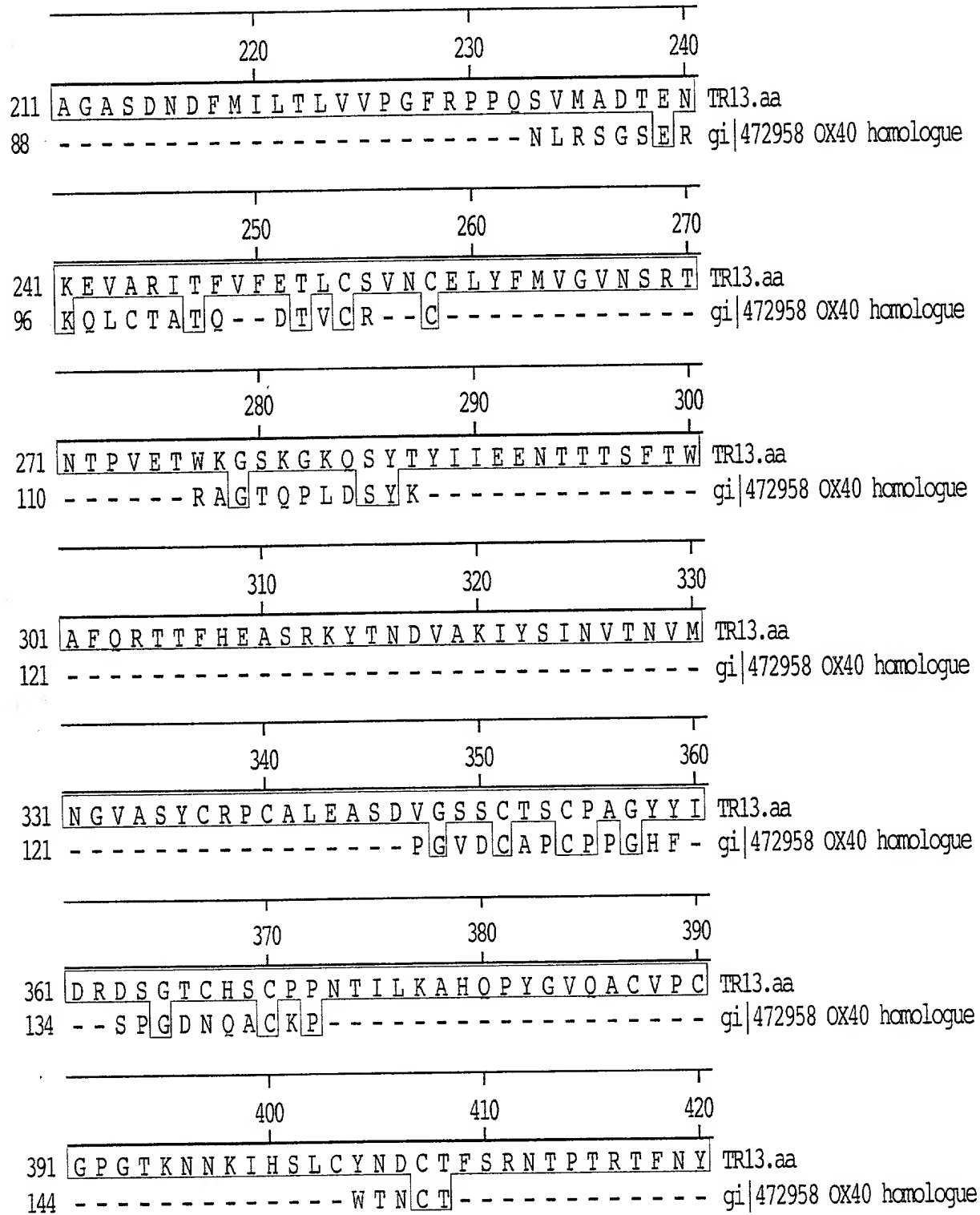


FIG. 2B

	430	440	450	
421	NFSALANTVTLAGGPSFTSKGLKYFHHFTL			TR13.aa
149	---LAKHTLQPASNSSD-----			gi 472958 OX40 homologue
	460	470	480	
451	SLCGNQGRKMSVCTDNVTDLRIP EGESGFS			TR13.aa
164	-----AICEDRDPPATQPEETQG--			gi 472958 OX40 homologue
	490	500	510	
481	KSITAYVCOAVIIPPEVTGYKAGVSSQPVSS			TR13.aa
182	-----PP-----ARPIIT			gi 472958 OX40 homologue
	520	530	540	
511	LADRLIGVTTDMTLDGITSPAELFHLES LG			TR13.aa
189	VQ-----PTEA-----			gi 472958 OX40 homologue
	550	560	570	
541	IPDVIFFYRSNDVTQSCSSGRSTTIRVRCSS			TR13.aa
195	-----			gi 472958 OX40 homologue
	580	590	600	
571	POKTVPGSLLLPGTCS DGTCDGCNHFHLEWE			TR13.aa
195	-----WP			gi 472958 OX40 homologue
	610	620	630	
601	SAAACP LCSVADYHAIVSSCVAGIQKTTYV			TR13.aa
197	RTSOGP-----			gi 472958 OX40 homologue

FIG. 2C

		640	650	660	
631	W R E P K L C S G G I S L P E O R V T I C K T I D F W L K V				TR13.aa
203	- - - - - S T R P V E V P G G R - A V A A I L G L G L V L				gi 472958 OX40 homologue
		670	680	690	
661	G I S A G T C T A I L L T V L T C Y F W K K N Q K L E Y K Y				TR13.aa
226	G L L G P L - - A I L L A L - - - Y L L R R D Q R L P P D A				gi 472958 OX40 homologue
		700	710	720	
691	S K L V M N A T L K D C D L P A A D S C A I M E G E D V E D				TR13.aa
251	H K P P G G G S F R - - - - - T P I Q E E Q A D A				gi 472958 OX40 homologue
		730	740	750	
721	D L I F T S K N H S L G R S N H L P P R G L L M D L T Q C R				TR13.aa
271	H S T L A - - - - - - - - - - - - - - - - - K				gi 472958 OX40 homologue
751					TR13.aa
277	I				gi 472958 OX40 homologue

FIG. 2D

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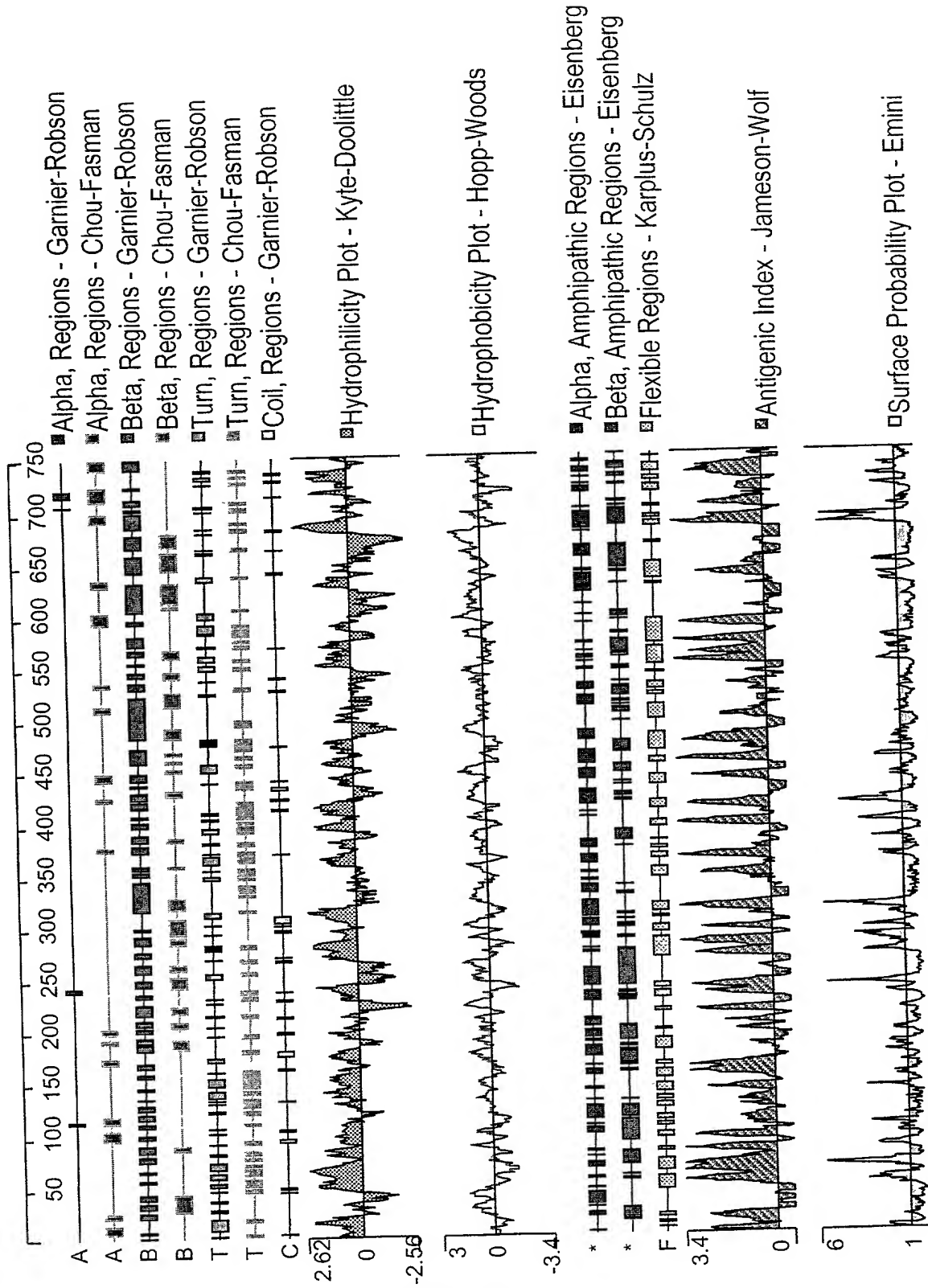


FIG. 3

1 TGAGGTGGATTGTACCGGAGTCCCATTGGGAGCAAGAGCCATCTACTCGTCCGTTACC 60

61 GGCCTTCCCACCATGGATTGCCAAGAAAATGAGTACTGGGACCAATGGGGACGGTGTGTC 120

1 M S T G T ~~N~~ C D G V S 11

121 ACCTGCCAACGGTGTGGTCCCTGGACAGGAGCTATCCAAGGATTGTGGTTATGGAGAGGGT 180

12 P A N G V V L D R S Y P R I V V M E R V 31

181 GGAGATGCCTACTGCACAGCCTGCCCTCCTCGCAGTACAAAAGCAGCTGGGGCCACCACA 240

32 E M P T A Q P A L L A V Q K Q L G P P Q 51

241 AATGTGCAGAGTTGCATGCACCTGTGCTGTCAATCGTTCAGAAGGTCAACTGCAC 300

52 M C R V A C T C A V I N R V Q K V N C T 71

301 ACCTACCTCTAATGCTGTCTGTGGGACTGTTTGCCAGGTTCTACCGAAAGACACGCAT 360

72 P T S N A V C G D C L P R F Y R K T R I 91

361 TGGAGGCCTGCAGGACCAAGAGTGCATCCCGTGCACGAAGCAGACCCCCACCTCTGAGGT 420

92 G G L Q D Q E C I P C T K Q T P T S E V 111

421 TCAATGTGCCTTCCAGTTGAGCTTAGTGGAGGCAGATGCACCCACAGTGCCCCCTCAGGA 480

112 Q C A F Q L S ~~L V E~~ A D A P T V P P Q E 131

481 GGCCACACTTGTTGCACTGGTGAGCAGCCTGCTAGTGGTGTACCTGGCCTTCCTGGG 540

132 A T L V A L V S S L L V V F T L A F L g 151

541 GCTCTTCTTCTCTACTGCAAGCAGTTCTTCAACAGACATTGCCAGCGTGGAGGTTTGCT 600

152 l f f l y c k q f f n r h c q r g g l l 171

601 GCAGTTTGAGGCTGATAAAACAGCAAAGGAGGAATCTCTTCCCCGTGCCACCCAGCAA 660

172 q f e a d k ~~t a k e~~ e s l f p v p p s k 191

FIG.4A

661 GGAGACCAGTGTCTGAGTCCCAAGTCTCTTGGGCCCCCTGGCAGCCTTGCCCAGTTGTTCTC 720
 192 e t ~~s a e~~ s q v s w a p g s l a q l f s 211
 721 TCTGGACTCTGTTCCCTATACCACAACAGCAGCAGGGCCCTGAAATGTGATGTCCACAAGA 780
 212 l d s v p i p q q q q g p e m * 227
 781 GCTAATACCCTACAGATGGGGCATATCCTATCCCATCCCACCAGAGGATTGATTCTCCAT 840
 841 TTCACAAGGACTGATCTGGAGCATTCTTGCTTCCTGTTGTAGTCTGGGGAGCCAGATT 900
 901 CCACATTCATGGGACTACCAGACATGTTCTAGCTCAACTTGATTATAGAGAAGAGGAGA 960
 961 GAGGACAGTGAATGGGGTAGGGTTTTTCATGTCTGCATTTTTGGTCAGGTAAGCCTCTCAA 1020
 1021 AATTGTGTTGCCACATCTACCTAGCACTTTAGGGACAAAATCAAACCCTTCTCCCCTTTT 1080
 1081 AGCTCCTCCCACTGCCTCCCTCCTCAACACACACACACACATACACACACATATACA 1140
 1141 TAGACACACAAACACACACACACACATTAATATCTATCTTGGGGGAAGCCTCGTGCCATA 1200
 1201 ATTCCCAAGTCATGTCTCAGACTGCTGCATTGCAGCATGACGCAGGGCAAACACTTTCCC 1260
 1261 TCTAGATCCCTGGGGCTTACCCTGTATTGAGGTTCTCACCACCCTCAGCAGGGAGAAG 1320
 1321 GGCTGAAGTTCGCCATTTTGGAACTTACAGAACATTTCTGAGCCAAAGTAATCTTCCTT 1380
 1381 CTGGGGCCTGAGTCCCCAACTACCCACAGCAGTCCCTCAAAGACAGCCCTCAATCCA 1440
 1441 TGTAGGGACATCTGAGTATGCCTCTTTCTATTGAAATGTCAATTCAATCCCAGCTTTCTC 1500
 1501 ACCACCGTTCCCCTTTGATTCTTTCTCAATTGTCTTTTTGCCTTTAGCTCCACCTATAC 1560

FIG.4B

1561 ATCTCATGCTCAGAGAAAAACAAGTTCCTTAGAGGTTGTATTCTTTATTCTCCAAGAATC 1620
 1621 TGTCTGAAACTTGTACAGCTAGTTCCTGTCCCACAACCTATTAAGTGGTTTATTAAGTACA 1680
 1681 TTAGGCAGAATGTGCACTTCATCACCAGGTTCTAGCTCTGGCAAAGGAGTGCTGTCTACA 1740
 1741 GCAAGATTTTTGCTTTTAGAATTTTATTAACACATCTTTTGGGTTTCATCCATCTACAAA 1800
 1801 CACTGATTAAGGGCCCCCTGGGGCAACCAATTGATCAGATTACTAAAAGGACTTGGGAAAA 1860
 1861 AGCAAAAAGGTCCCATTGTACTGGACTGAGGATTAGAAGCAATTGAAATACAAGCCTGTA 1920
 1921 CCAAGCAAGCAGCCTGGCCCCACACAGGTATTAGCAAATATGTGGTAACCAAGGTTTTAG 1980
 1981 GCCTTGGCCCCCTAGGTTTCCTGTTTTTTTTTCGTTTTGGTTTTCCGTTTTTCGTTTTTGA 2040
 2041 ACAGGTATTCTTATCTCACTGGCTTTCCTGATCATGTTTAGACCTTCTGGTAGAAGAA 2100
 2101 ATAATATCCAGACAGGGGATGATTTGGCTTCAGCAGGCTGCAGGTGTTCAAAGGTTGCCA 2160
 2161 TGTGGCTGGCAGTGGTTCAAGCCACATTTGACACTGCTGCTCTAGAGGAAAGATAATGA 2220
 2221 TGGTAACACAGTAATAATAATAATAACAAAAATATGATAAAGTGAAAGAGTAGATTT 2280
 2281 CTTTCAGTGTGCTTGCTCCATGGCATGAATGCTATGTGGACAGCCCAAGCCATACCCAGA 2340
 2341 ATCACCTTAATTCCTAACTTTTTGAGGTTGAGCAATTGGAGGTGGCAATTGGCTTTGCATT 2400
 2401 TTAAAGTATTTGGGTAAAGGTGAAGTGAAGGATTTTCCTCTTTATAATTTCTGTTTGGC 2460
 2461 CATGGCAAATACCATAGTTGAGTATTTGCTTCAGGAGAGTTCTTTTACAGTTTACTTT 2520

FIG.4C

2521 TCAATGCTGAGGCATATTTCTTTGAGCACTGTGCTTTTATGTGTCTTTCTACAAAGGGGT 2580

2581 TATTGGTCAGTGAAGAACAAGTACACTTGATAAAAACATTTTCAACATACATTGAGCC 2640

2641 TAAACAGCAGTTAAGTTGTCTCTAATGAAGTAGCAAAAAAAAAAAATGTAGTTTTTGTTC 2700

2701 GTAAGGAAGGGGAGGTATTTCTGAGAATGAATTTTTTTTTTTTGGATTACTGTTTTTC 2760

2761 TCTCCATATACCTTGACTTGGATTTTGACAGGAGGGAGTCTGGGAAAATAATTTTTTCCT 2820

2821 CCAAGATTCTCAGATCCAGGTTAGGAAAGGATTCAGCACTACAGCATACCCCTCTACAAC 2880

2881 ATACAGCCCTGTCACATTGAGATCATAATCCCTCCTGTCCCACTCCTCTCTACCAACCCC 2940

2941 ACCCTACTAGCTAGGTCTTCAGTGTTTTACATTGAATATTGGTACATTTTAATTATTTTT 3000

3001 TCTCATAAATGGGTATTTATAGAGATTTTGTAACTCTTGAGCCATATGCATGTGTAGA 3060

3061 TACTGGCAGGCCTATGTTTGTATGATGCTCTGCAAACATTTTATATTGGCCAATAAAC 3120

3121 AGAAATATATCCAAAAAAAAAAAAAAAAAtnRmssngsgnatdATGGATTGCCAAGAA 3180

3181 AATGAGTACTGGGACCAATGGGGACGGTGTGTACCTGCCAACGGTGTGGTCCTGGACAG 3240

3241 GAGCTATCCAAGGATTGTGGTTATGGAGAGGGTGAGATGCCTACTGCACAGCCTGCCCT 3300

3301 CCTCGCAGTACAAAAGGCAGCTGGGGCCACCACAAATGTCAGAGTTGCATCACCTGTGCT 3360

3361 GTCATCAATCGTGTTCAGAAGGTCAACTGCACAGCTACCTCTAATGCTGTCTGTGGGGAC 3420

3421 TGTTTGCCAGGTTCTACCGAAAGACACGCATTGGAGGCCTGCAGGACCAAGAGTGCATC 3480

FIG.4D

3481 CCGTGCACGAAGCAGACCCCCACCTCTGAGGTTCAATGTGCCTTCCAGTTGAGCTTAGTG 3540
3541 GAGGCAGATGCACCCACAGTGGCCCCCTCAGGAGGCCACACTTGTTGCACTGGTGAGCAGC 3600
3601 CTGCTAGTGGTGTGTTTACCCTGGCCTTCCTGGGGCTCTTCTTCCTCTACTGCAAGCAGTTC 3660
3661 TTCAACAGACATTGCCAGCGTGGAGGTTTGCTGCAGTTTGAGGCTGATAAAACAGCAAAG 3720
3721 GAGGAATCTCTCTTCCCCGTGCCACCCAGCAAGGAGACCAGTGCTGAGTCCCAAGTCTCT 3780
3781 TGGGCCCCTGGCAGCCTTGCCCAGTTGTTCTCTCTGGACTCTGTTCCCTATACCACAACAG 3840
3841 CAGCAGGGGCCTGAAATGTGA 3861

FIG.4E

FIG. 5A

FIG. 5A

	10	20	30																																			
1	M	S	T	G	T	N	G	D	G	V	S	P	A	N	G	V	V	L	D	R	S	Y	P	R	I	V	V	M	E	R	TR14.aa							
1	M	A	P	V	A	-	-	-	-	V	W	A	A	L	A	V	G	L	E	L	W	A	A	H	A	L	P	A	Q	gi 339758 Tumor Necrosis Factor								
	40	50	60																																			
31	V	E	M	P	-	-	T	A	O	P	A	L	L	A	V	O	K	O	L	-	-	G	P	P	Q	M	C	R	V	A	TR14.aa							
27	V	A	F	T	P	Y	A	P	E	P	G	S	T	C	R	L	R	E	Y	Y	D	Q	T	A	Q	M	C	C	S	K	gi 339758 Tumor Necrosis Factor							
	70	80	90																																			
57	C	T	C	A	V	I	N	R	V	O	K	V	N	C	T	P	T	S	N	A	V	C	G	D	C	L	P	R	F	Y	TR14.aa							
57	C	S	P	G	-	-	-	Q	H	A	K	V	F	C	T	K	T	S	D	T	V	C	D	S	C	E	D	S	T	Y	gi 339758 Tumor Necrosis Factor							
	100	110	120																																			
87	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	TR14.aa							
84	T	Q	L	W	N	W	V	P	E	C	L	S	C	G	S	R	C	S	S	D	Q	V	E	T	Q	A	C	T	R	E	gi 339758 Tumor Necrosis Factor							
	130	140	150																																			
87	-	-	-	-	-	-	-	-	-	R	K	T	R	I	G	G	L	Q	D	Q	E	-	-	-	-	-	-	-	-	-	-	TR14.aa						
114	Q	N	R	I	C	T	C	R	P	G	W	Y	C	A	L	S	K	Q	E	G	C	R	L	C	A	P	L	R	K	C	gi 339758 Tumor Necrosis Factor							
	160	170	180																																			
99	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	C	I	P	C	T	K	Q	T	-	-	-	-	TR14.aa						
144	R	P	G	F	G	V	A	R	P	G	T	E	T	S	D	V	V	C	K	P	C	A	P	G	T	F	S	N	T	T	gi 339758 Tumor Necrosis Factor							
	190	200	210																																			
107	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	P	T	S	E	V	Q	C	A	-	-	-	TR14.aa							
174	S	S	T	D	I	C	R	P	H	Q	I	C	N	V	V	A	I	P	G	N	A	S	R	D	A	V	C	T	S	T	gi 339758 Tumor Necrosis Factor							
	220	230	240																																			
115	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	F	Q	L	S	L	V	E	A	D	A	P	T	V	P	P	O	E	A	TR14.aa
204	S	P	T	R	S	M	A	P	G	A	V	H	L	P	Q	P	V	S	T	R	S	Q	H	T	Q	P	T	P	E	P	gi 339758 Tumor Necrosis Factor							

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FIG. 5B

133 TLVALVSSLLVV - - - - - FT L A F - TR14.aa
 234 STAPST[S]FLLPMGSPSPAEGSTGD[F]A[L]PVG gi|339758 Tumor Necrosis Factor

150 - - - - - LGLFFL - - - YCKOFFNRH - - - C TR14.aa
 264 LIVGVTA[LGL]LIIGVVN[C]VIMTQVKKKPL[C] gi|339758 Tumor Necrosis Factor

166 - QRGGLL - QFEADKT - - - - - AKEESLFPVP TR14.aa
 294 LQREAKVPHLP[ADK]ARGTQGP EQQLLITA gi|339758 Tumor Necrosis Factor

189 PSK - - - - - TR14.aa
 324 PS[SSSSSS]LESSASALDRRAPTRNQPPQAPGV gi|339758 Tumor Necrosis Factor

192 - - - - - TR14.aa
 354 EASGAGEARASTGSSDSSPGGHGTQVNVTC gi|339758 Tumor Necrosis Factor

192 - - - - - TR14.aa
 384 IVNVCSSSDHSSQCSSQASSTMGDTDSSPS gi|339758 Tumor Necrosis Factor

192 ETSAESQVSWA - - - - - PGS LAQL TR14.aa
 414 E[SPKDE]QVPFSKEECAFRSQLETP[E]T[L]LGS gi|339758 Tumor Necrosis Factor

460
 120 FSLDSVPIPOQQQGP[EM] TR14.aa
 444 TEEKPL[P]LGVPDA[G]MKPS gi|339758 Tumor Necrosis Factor

"C" = Cysteine
 "E" = Glutamic acid
 "F" = Phenylalanine
 "G" = Glycine
 "H" = Histidine
 "I" = Isoleucine
 "K" = Lysine
 "L" = Leucine
 "M" = Methionine
 "P" = Proline
 "Q" = Glutamine
 "R" = Arginine
 "S" = Serine
 "T" = Threonine
 "V" = Valine
 "W" = Tryptophan
 "Y" = Tyrosine

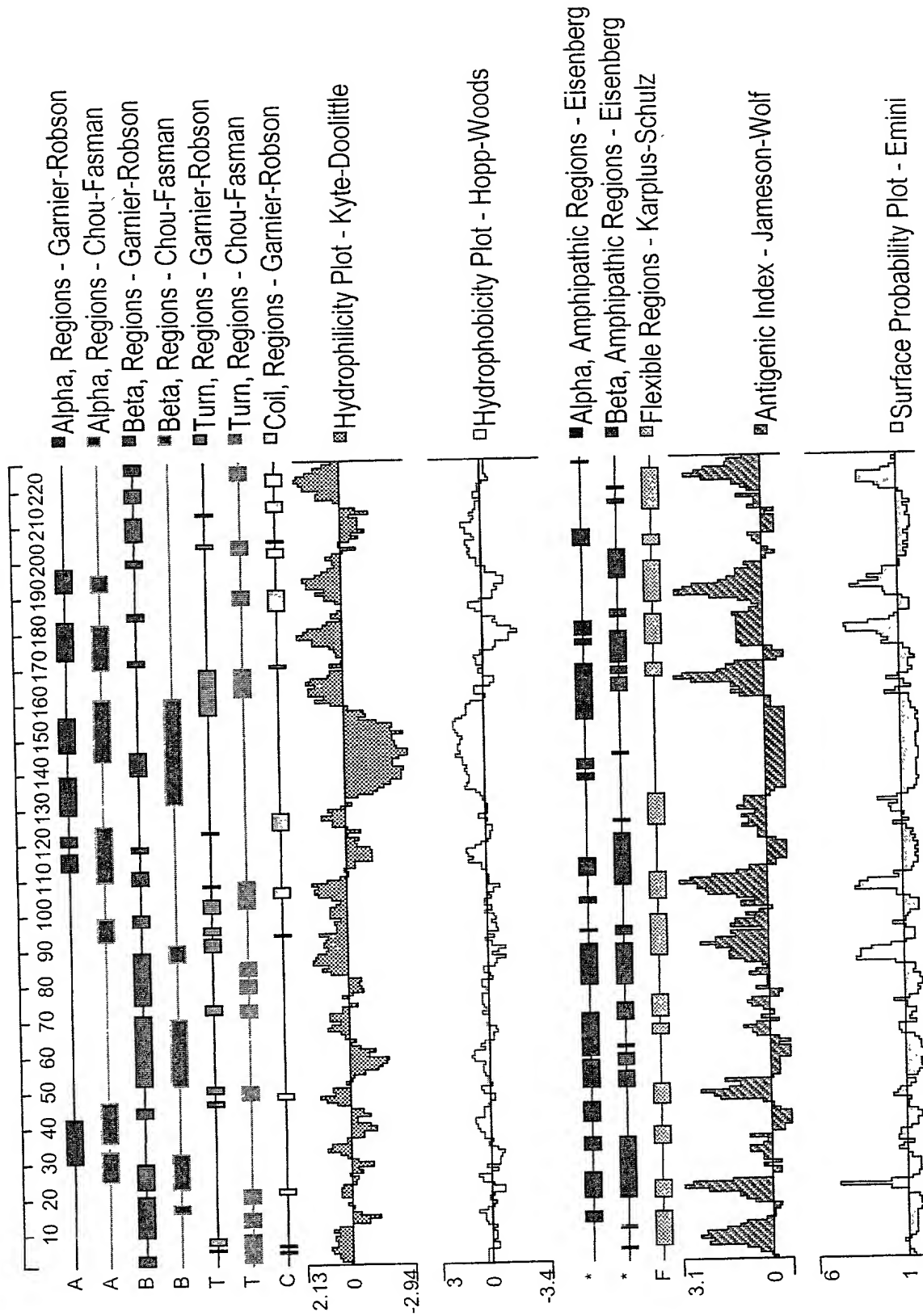


FIG. 6

1 GCAGAAGCAGCAGCCGAGCACCTGAGCCGCTACTGCCGCTCACTCAGGACAACGCTATG 60
 1 M 1

 61 GCTGAGCCTGGGCACAGCCACCATCTCTCCGCCAGAGTCAGGGGAAGAACTGAGAGGCGC 120
 2 A E P G H S H H L S A R V R G R T E R R 21
 121 ATACCCCGGCTGTGGCGGCTGCTGCTCTGGGCTGGGACCGCCTTCCAGGTGACCCAGGGA 180
 22 I P R L W R L L L W A G T A F Q V T Q G 41
 181 ACGGGACCGGAGCTTCACGCCTGCAAAGAGTCTGAGTACCACTATGAGTACACGGCGTGT 240
 42 T G P E L H A C K E S E Y H V E Y T A C 61
 ++++++
 241 GACAGCACGGGTTCCAGGTGGAGGGTCGCCGTGCCGCATACCCCGGGCCTGTGCACCAGC 300
 62 D S T G S R W R V A V P H T P G L C T S 81
 + ++++++
 301 CTGCCTGACCCCGTCAAGGGCACCGAGTGCTCCTTCTCCTGCAACGCCGGGAGTTTCTG 360
 82 L P D P V K G T E C S F S C N A G E F L 101

 361 GATATGAAGGACCACTCATGTAAGCCATGCGCTGAGGGCCGCTACTCCCTCGGCACAGGC 420
 102 D M K D Q S C K P C A E G R V S L G T G 121
 421 ATTCCGTTTGTATGAGTGGGATGAGCTGCCCCATGGCTTTGCCAGCCTCTCAGCCAACATG 480
 122 I R F D E W D E L P H G F A S L S A N M 141
 .+++++*****.
 481 GAGCTGGATGACAGTCTGCTGAGTCCACCGGGAAGTGTACTTCGTCCAAGTGGGTTCCTC 540
 142 E L D D S A A E S T G N C T S S K W V P 161
 541 CGGGGCGACTACATCGCCTTCAACACGGACGAATGCACAGCCACACTGATGTACGCCGTC 600
 162 R G D Y I A F N T D E C T A T L M Y A V 181
 601 AACCTGAAGCAATCTGGCACCGTTAACTTCGAATACTACTATCCAGACTCCAGCATCATC 660
 182 N L K Q S G T V N F E Y Y Y P D S S I I 201

FIG. 7A

661 TTTGAGTTTTTCGTTTCTCAGAATGACCAGTGGCCAGCCCAATGCAGATGACTCCAGGTGGATG 720
 202 F E F F V Q N D Q C Q P N A D D S R W M 221

 721 AAGACCACAGAGAAAGGATGGGAATTCACAGTGTGGAGCTAAATCGAGGCAATAATGTC 780
 222 K T T E K G W E F H S V E L N R G N N V 241
 .
 781 CTCTATTGGAGAACCACAGCCTTCTCAGTATGGACCAAAGTACCCAAGCCTGTGCTGGTG 840
 242 L Y W R T T A F S V W T K V P K P V L V 261
 .
 ++++++
 841 AGAAACATTGCCATAACAGGGGTGGCCTACACTTCAGAATGCTTCCCCTGCAAACCTGGC 900
 262 R N I A I T G V A Y T S E C F P C K P G 281
 .
 ++++++
 901 ACGTATGCAGACAAGCAGGGCTCCTCTTTCTGCAAACCTTGCCAGCCAACTCTTATTCA 960
 282 ~~T~~ Y A ~~D~~ K Q G S S F C K L C P A N S Y S 301
 .
 ***** ++++
 961 AATAAAGGAGAACTTCTTGCCACCAGTGTGACCCTGACAAATACTCAGAGAAAGGATCT 1020
 302 N K G E T S C H Q C D P D K Y S E K G S 321
 ++++++ *****
 1021 TCTTCTGTAACTGCGCCAGCTTGCACAGACAAAGATTATTTCTACACACACACGGCC 1080
 322 S S C N V R P A C ~~T~~ ~~D~~ ~~K~~ ~~D~~ Y F Y T H ~~T~~ A 341
 .
 1081 TGCGATGCCAACGGAGAGACACAACCTCATGTACAAATGGGCCAAGCCGAAAATCTGTAGC 1140
 342 ~~C~~ ~~D~~ A N G E T Q L M Y K W A K P K I C S 361
 .
 1141 GAGGACCTTGAGGGGGCAGTGAAGCTGCCTGCCTCTGGTGTGAAGACCCACTGCCCACCC 1200
 362 E D L E G A V K L P A S G V K T H C P P 381
 .
 ++++++
 1201 TGCAACCCAGGCTTCTTCAAAACCAACAACAGCACCTGCCAGCCCTGCCCATATGGTTCC 1260
 382 C N P G F F K T N N S T C Q P C P Y G S 401
 ++++++ ++++++
 1261 TACTCCAATGGCTCAGACTGTACCCGCTGCCCTGCAGGGACTGAACCTGCTGTGGGATTT 1320
 402 Y S N G S D C T R C P A G T E P A V G F 421

FIG. 7B

1321 GAATACAAATGGTGAACACGCTGCCACAAACATGGAACGACCGTTCTCAGTGGGATC 1380
 422 E Y K W W N T L P T ~~N M~~ E T T V L S G I 441
 1381 AACTTCGAGTACAAGGGCATGACAGGCTGGGAGGTGGCTGGTGATCACATTTACACAGCT 1440
 442 N F E Y K G M T ~~C W~~ E V A G D H I Y T A 461
 ++++++.
 1441 GCTGGAGCCTCAGACAATGACTTCATGATTCTCACTCTGGTTGTGCCAGATTAGACCT 1500
 462 A G A S ~~D N~~ D F M I L T L V V P G F R P 481
 1501 CCGCAGTCCGTGATGGCAGACACAGAGAATAAAGAGGTGGCCAGAATCACATTTGTCTTT 1560
 482 P Q S V M A D T E N K E V A R I T F V F 501
 1561 GAGACCCTCTGTTCTGTGAAGTGTGAGCTCTACTTCATGGTGGGTGTGAATTCTAGGACC 1620
 502 E T L C S V N C E L Y F M V G V N S R T 521
 *****
 1621 AACACTCCTGTGGAGACGTGGAAAGGTTCCAAAGGCAAACAGTCCTATACCTACATCATT 1680
 522 N T ~~P V~~ E T W K G S K G K Q S Y T Y I I 541
 1681 GAGGAGAACTACCACGAGCTTACCTGGGCCTTCCAGAGGACCACTTTTCATGAGGCA 1740
 542 E E N T T T S F T W A F Q R T T ~~F H~~ E A 561
 *****
 1741 AGCAGGAAGTACACCAATGACGTTGCCAAGATCTACTCCATCAATGTCACCAATGTTATG 1800
 562 S R K Y T N D V A K I Y S I N V T N V M 581
 ++++++ .
 1801 AATGGCGTGGCCTCCTACTGCCGTCCTGTGCCCTAGAACCTCTGATGTGGGCTCCTCC 1860
 582 N G V A S Y C R P C A L E A S D V G S S 601
 ++++++ ++++++.
 1861 TGCACCTCTTGTCTGCTGGTTACTATATTGACCGAGATTCAGGAACCTGCCACTCCTGC 1920
 602 C T S C P A G Y Y I D R D S G T C H S C 621
 ++++++.
 1921 CCCCCTAACACAATTCTGAAAGCCCACCAGCCTTATGGTGTCCAGGCCTGTGTGCCCTGT 1980
 622 P P N T I L K A H Q P Y G V Q A C V P C 641

FIG. 7C

++++++
 1981 GGTCCAGGACCAAGAACAACAAGATCCACTCTCTGTGCTACAATGATTGCACCTTCTCA 2040
 642 G P G T K N N K I H S L C Y N D C T F S 661

 2041 CGCAACACTCCAACCAGGACTTTCAACTACAACCTTCTCGCTTTGGCAAACACCGTCACT 2100
 662 R N T P T R T F N Y N F S A L A N T V T 681

 2101 CTTGCTGGAGGGCCAAGCTTCACTTCCAAAGGGTTGAAATACTTCCATCACTTTACCTC 2160
 682 L A G G P S F T S K G L K Y F H H F T L 701

 2161 AGTCTCTGTGGAACCAAGGGTAGGAAAATGTCTGTGTGCACCGACAATGTCACTGACCTC 2220
 702 S L C G N Q G R K M S V C T D N V T D L 721

 2221 CGGATTCCTGAGGGTGAGTCAGGGTTCTCCAATCTATCACAGCCTACGTCTGCCAGGCA 2280
 722 R I P E G E S G F S K S I T A Y V C Q A 741

 2281 GTCATCATCCCCCAGAGGTGACAGGCTACAAGGCCGGGGTTTCCTCACAGCCTGTCAGC 2340
 742 V I I P P E V T G Y K A G V S S Q P V S 761

 2341 CTTGCTGATCGACTTATTGGGGTGACAACAGATATGACTCTGGATGGAATCACCTCCCCA 2400
 762 ~~L A D~~ R L I G V T T D M T L D G I T S ~~P~~ 781

 2401 GCTGAACCTTTTCCACCTGGAGTCCTTGGGAATACCGGACGTGATCTTCTTTTATAGGTCC 2460
 782 ~~A E~~ L F H L E S L G I P D V I F F Y R S 801

 2461 AATGATGTGACCCAGTCCTGCAGTTCTGGGAGATCAACCACCATCCGCGTCAGGTGCAGT 2520
 802 N D V T Q S C S S G R S T T I R V R C S 821

 2521 CCACAGAAACTGTCCCTGGAAGTTTGCTGCTGCCAGGAACGTGCTCAGATGGGACCTGT 2580
 822 P Q K T V P G S L L L P G ~~T C S D~~ G T C 841
 ++++++
 2581 GATGGCTGCAACTTCCACTTCTGTGGGAGAGCGGGCTGCTTGCCCGCTCTGCTCAGTG 2640
 842 D G C N F H F L W E S A A A C P L C S ~~V~~ 861

FIG. 7D

. ++++++ .
 2641 GCTGACTACCATGCTATCGTCAGCAGCTGTGTGGCTGGGATCCAGAAGACTACTTACGTG 2700
 862 A—D Y H A I V S S C V A G I Q K T T Y V 881

 2701 TGGCGAGAACCCAAGCTATGCTCTGGTGGCATTCTCTGCCTGAGCAGAGATCACCATC 2760
 882 W R E P K L C S G G I S—L—P—E Q R V T I 901
 ++++++ .
 2761 TGCAAAACCATAGATTTCTGGCTGAAAGTGGGCATCTCTGCAGGCACCTGTACTGCCATC 2820
 902 C K T I D F W L K V G I S A G T C T A I 921

 2821 CTGCTCACCGTCTTGACCTGCTACTTTTGGAAAAAGAATCAAAAAGTAGAGTACAAGTAC 2880
 922 L L T V L T C Y F W k k n q k l e y k y 941
 ***** .
 2881 TCCAAGCTGGTGATGAATGCTACTCTCAAGGACTGTGACCTGCCAGCAGCTGACAGCTGC 2940
 942 s k l v m n a t—l—k—d c d l p a a d s c 961
 ***** .
 2941 GCCATCATGGAAGGCCAGGATGTAGAGCAGCCTCATCTTTACCAGCAAGAATCACTCT 3000
 962 a i m e g e d v e d d l i f t . s k n h s 981

 3001 TTGGGAAGATCAAATCATTTACCTCCAAGAGGACTCCTGATGGATTTGACTCAGTGCCGC 3060
 982 l g r s n h l p p r g l l m d l t q c r 1001

 3061 TGAAGACATCCTCAGGAGGCCAGACATGGACCTGTGAGAGGCACTGCCTGCCTCACCTG 3120
 1002 * 1002

 3121 CCTCCTCACCTTGCCATAGCACCTTTGCAAGCCTGCGGCGATTGGGTGCCAGCATCCTGC 3180

 3181 AACACCCACTGCTGGAAATCTCTTCATTGTGGCCTTATCAGATGTTTGAATTCAGATCT 3240

 3241 TTTTTATAGAGTACCCAAACCCTCCTTTCTGCTTGCCCTCAAACCTGCCAAATATACCCA 3300

 3301 CACTTTGTTTGTAAATTAATAAAAAAAAAAAAAAAAAA 3334

FIG. 7E

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FIG. 8A

		10	20	30	
1	M A E P G H S H L S A R V R G R T E R R I P R L W R L L L	TR13-alpha.aa			
1	M - - - - -	gb AAB94382.1 TNF Receptor II			
		40	50	60	
31	W A G T A F O V T O G T G P E L H A C K E S E Y H Y E Y T A	TR13-alpha.aa			
2	- - - - - K S V L Y S Y I L - -	gb AAB94382.1 TNF Receptor II			
		70	80	90	
61	C D S T G S R W R V A V P H T P G L C T S L P D P V K G T E	TR13-alpha.aa			
11	- - - - -	gb AAB94382.1 TNF Receptor II			
		100	110	120	
91	C S F S C N A G E F L D M K D O S C K P C A E G R Y S L G T	TR13-alpha.aa			
11	- - - - - F L - - - - - S C - - - - -	gb AAB94382.1 TNF Receptor II			
		130	140	150	
121	G I R F D E W D E L P H G F A S L S A N M E L D D S A A E S	TR13-alpha.aa			
15	- I I I N G R D V A P Y - - - - - A P S	gb AAB94382.1 TNF Receptor II			
		160	170	180	
151	T G N C T S S K W V P R G D Y I A F N T D E C T A T L M Y A	TR13-alpha.aa			
29	N G K C K D N E - - - - -	gb AAB94382.1 TNF Receptor II			
		190	200	210	
181	V N L K O S G T V N F E Y Y P D S S I I F E F F V O N D O	TR13-alpha.aa			
37	- - - - - Y N R H N L	gb AAB94382.1 TNF Receptor II			
		220	230	240	
211	C O P N A D D S R W M K T T E K G W E F H S V E L N R G N N	TR13-alpha.aa			
43	C - - - - -	gb AAB94382.1 TNF Receptor II			
		250	260	270	
241	V L Y W R T T A F S V W T K V P K P V L V R N I A I T G V A	TR13-alpha.aa			
44	- - - - -	gb AAB94382.1 TNF Receptor II			

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FIG. 8B

271	Y T S E C F P C K P G T Y A D K Q G S S F C K L C P A N S Y	TR13-alpha.aa
44	- - - - C L S C P P G T Y A S R - - - - - L C D S K T -	gb AAB94382.1 TNF Receptor II
301	S N K G E T S C H O C D P D K Y S E K G S S S C N V R P A C	TR13-alpha.aa
62	- - N T N T Q C T P C G S D T F T S R N N H L - - - - P A C	gb AAB94382.1 TNF Receptor II
331	T D K D Y F Y T H T A C D A N G E T O L M Y K W A K P K I C	TR13-alpha.aa
86	- - - - - L S C N G R C D S N Q V E T R S C N T T H N R I C	gb AAB94382.1 TNF Receptor II
361	S E D L E G A V K L P A S G V K T H C P P C N P G F F K T N	TR13-alpha.aa
111	D - - - - - - - - - - - - - - - C A P G Y Y - - -	gb AAB94382.1 TNF Receptor II
391	N S T C O P C P Y G S Y S N G S D C T R C P A G T E P A V G	TR13-alpha.aa
118	- - - - - C L L - - - - K G S G C K A C V S Q T K C G I G	gb AAB94382.1 TNF Receptor II
421	F E Y K W W N T L P T N M E T T V L S G I N F E Y K G M T G	TR13-alpha.aa
138	Y - - - - - - - - - - - - - - - G V S G	gb AAB94382.1 TNF Receptor II
451	W E V A G D H I Y T A A G A S D N D F M I L T L V V P G F R	TR13-alpha.aa
143	H T P T G D V I - - - - - - - - - - - - - - -	gb AAB94382.1 TNF Receptor II
481	P P O S V M A D T E N K E V A R I T F V F E T L C S V N C E	TR13-alpha.aa
151	- -	gb AAB94382.1 TNF Receptor II
511	L Y F M V G V N S R T N T P V E T W K G S K G K Q S Y T Y I	TR13-alpha.aa
151	- -	gb AAB94382.1 TNF Receptor II

FIG. 8C

541	I E E N T T T S F T W A F O R T T F H E A S R K Y T N D V A	TR13-alpha.aa
151	-----	gb AAB94382.1 TNF Receptor II
571	K I Y S I N V T N V M N G V A S Y C R P C A L E A S D V G S	TR13-alpha.aa
151	-----C S P C G L-----	gb AAB94382.1 TNF Receptor II
601	S C T S C P A G Y Y I D R D S G T C H S C P P N T I L K A H	TR13-alpha.aa
157	-----G T Y-----S H	gb AAB94382.1 TNF Receptor II
631	O P Y G V O A C V P C G P G T K N N K I H S L C Y N D C T F	TR13-alpha.aa
162	T V S S A D K C E P-----	gb AAB94382.1 TNF Receptor II
661	S R N T P T R T F N Y N F S A L A N T V T L A G G P S F T S	TR13-alpha.aa
172	---V P S N T F N Y-----I D V E I N L-----Y P V	gb AAB94382.1 TNF Receptor II
691	K G L K Y F H H F T L S L C G N O G R K M S V C T - D N V T	TR13-alpha.aa
190	N D-----T S C T R T T T T	gb AAB94382.1 TNF Receptor II
720	D L R I P E G E S G F S K S I T A Y V C O A V I I P P E V T	TR13-alpha.aa
201	G L S E S I S T S E L T I T M N H K D C D P V-----	gb AAB94382.1 TNF Receptor II
750	G Y K A G V S S O P V S L A D R L I G V T T D M T L D G I T	TR13-alpha.aa
224	- F R D G Y F S-----V L N K V A	gb AAB94382.1 TNF Receptor II
780	S P A E L F H L E S L G I P D V I F F Y R S N D V T Q S C S	TR13-alpha.aa
237	T S G-----F F T G E N R Y Q N T S	gb AAB94382.1 TNF Receptor II

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FIG. 8D

810	SGRSTTIRVRCSPQKTVPGLLLPGTCS DG	TR13-alpha.aa
252	NVCTLNFEIKC N N K D S S S K Q L - - - - -	gb AAB94382.1 TNF Receptor II
840	TC D G C N F H F L W E S A A A C P L C S V A D Y H A I V S	TR13-alpha.aa
273	- - - - - T K T K N D T I M P H S E T V T L V G	gb AAB94382.1 TNF Receptor II
870	S C V A G I O K T T Y V W R E P K L C S G G I S L P E O R V	TR13-alpha.aa
292	D C L S S V D - - I Y I - - - - L Y S N T - - - - -	gb AAB94382.1 TNF Receptor II
900	T I C K T I D F W L K V G I S A G T C T A I L L T V L T C Y	TR13-alpha.aa
307	- - - N T Q D Y - - - - -	gb AAB94382.1 TNF Receptor II
930	F W K K N O K L E Y K Y S K L V M N A T L K D C D L P A A D	TR13-alpha.aa
312	- - - E T D T I S Y H A G N V L - - - - - D V D S H M P G	gb AAB94382.1 TNF Receptor II
960	S C A I M E G E D V E D D L I F T S K N H S L G R S N H L P	TR13-alpha.aa
333	S C D I - - - - - H K L I T N S Q N P	gb AAB94382.1 TNF Receptor II
990	P R G L L M D L T Q C R	TR13-alpha.aa
347	T H - - - - - F L	gb AAB94382.1 TNF Receptor II

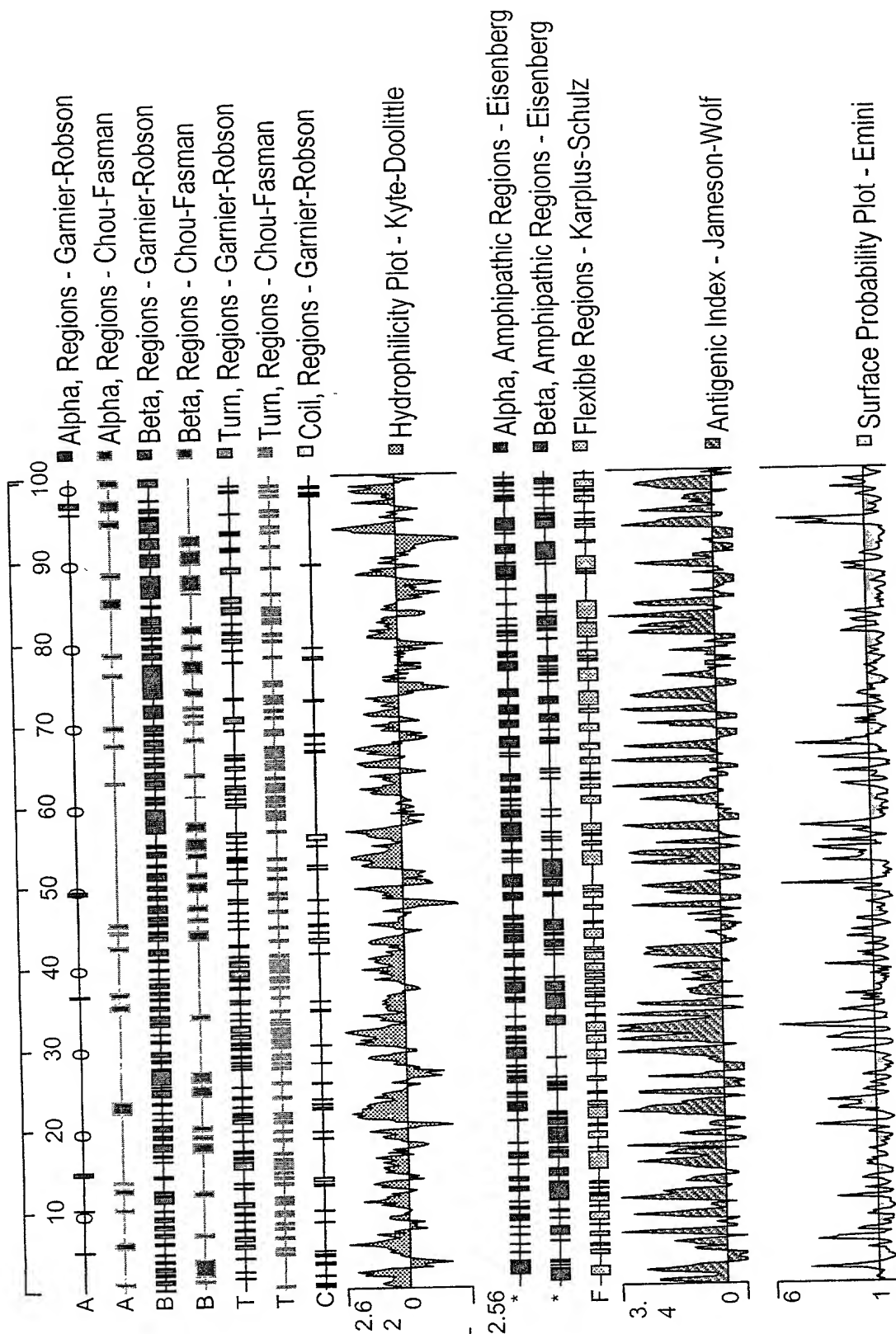


FIG. 9

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1	GGATTGTACCGGAGTCCCATTTGGGAGCAAGAGCCATCTACTCGTCCGTTACCGGCCTT	60
61	CCCACCATGGATTGCCAAGAAATGAGTACTGGGACCAATGGGACGGTGTGTCAACCTGC	120
1	M D C Q E N E Y W D Q W G R C V T C	18
121	CAACGGTGTGGTCCCTGGACAGGAGCTATCCAAGGATTGTGGTTATGGAGAGGTTGGAGAT	180
19	Q R C G P G Q E L S K D C G Y G E G D	38
181	GCCTACTGGCACAGCCTGCCCTCCTCGCAGTACAAAGCAGCTGGGGCCACCACAAATGT	240
39	A Y W H S L P S S Q Y K S S W G H H K C	58
241	CAGAGTTGCATCACCTGTGCTGTCAATCGTGTTCAGAAGGTCAACTGCACACCTACC	300
59	Q S C I T C A V I N R V Q K V N C T P T	78

FIG. 10A

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301	TCTAATGCTGCTGTGGGACTGTTTGCCAGGTTCTACCGAAAGACACGCATTTGGAGGC	360
79	S N A V C G D C L P R F Y R K T R I G G	98
361	CTGCAGGACCAAGAGTGCATCCCGTGCACGAAGCAGACCCCCACCTCTGAGGTTCAATGT	420
99	L Q D Q E C I P C T K Q T P T S E V Q C	118
421	GCCTTCCAGTTGAGCTTAGTGGAGGCAGATGCACCCACAGTGCCCCCTCAGGAGGCCACA	480
119	A F Q L S L V E A D A P T V P P Q E A T	138
481	CTTGTTGCACTGGTGAGCAGCCCTGCTAGTGGTGTATTACCCCTGGCCCTTCCTGGGGCTCTTC	540
139	<u>L V A L V S S L L V V F T L A F L G L F</u>	158
541	TTCCTCTACTGCAAGCAGTTCTTCAACAGACATTGCCAGCGTGGAGGTTTGCCTGCAGTTT	600
159	F L Y C K Q F F N R R H C O R G G L L Q F	178

FIG. 10B

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601 GAGGCTGATAAACAGCAAAGGAGGAATCTCTCTTCCCGTGCCACCCAGCAAGGAGACC 660
 179 E A D K T A K E E S L F P V P P S K E T 198

 661 AGTGTGAGTCCCAAGTCCTTGGGCCCCCTGGCAGCCTTGCCCCAGTTGTTCTCTCTGGAC 720
 199 S A E S Q V S W A P G S L A Q L F S L D 218

 721 TCTGTTCCTATACCACAACAGCAGAGGGGCCCTGAAATGTGATGTCCACAAGAGCTAATA 780
 219 S V P I P Q Q Q Q G P E M * 232

 781 CCTACAGATGGGCATATCCTATCCCATCCCAACAGAGGATTGATTCCTCCATTTCACAA 840

 841 GGACTGATCTGGAGCATTCTTGCTTCCCTGTGTAGTCTGGGAGCCAGATTCCACATT 900

 901 CATGGGACTACCAGACATGTTCCCTAGCTCAACTTGATTATAGAGAAGAGGAGAGGAGACA 960

FIG. 10C

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961	GTGAATGGGTAAGGTTTTCATGTCCTGCAATTTTGGTCAGGTAAGCCCTCTCAAAATTGTG	1020
1021	TTGGCACATCTACCTAGCACCTTTAGGGACAATAACAAACCTTCTCCCCCTTTTAGCTCCT	1080
1081	CCACACTGCCCTCCCTCCTCAACACACACACACATACACACACATATACATAGACAC	1140
1141	ACAAACACACACACACATTAATATCTATCTTGGGGGAAGCCCTCGTGCCATAATTCCCA	1200
1201	AGTCATGTCCTCAGACTGCTGCATTCAGCATGACGAGGGCAACACTTTCCTCTAGAT	1260
1261	CCCTGGGGCCCTCACCCCTGTATTTGAGGTTCTCACCCACCTCAGCAGGAGAGGGCTGAA	1320
1321	GTTCCGCCATTTTGGAACCTTACAGAACAATTTCTGAGCCAAAGTAATCTTCCTTCTGGGGC	1380

FIG. 10D

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1381	CTGAGT	TCCCCA	AACTAC	CCCCAC	AGCAGT	CCCTCA	AAAGAC	AGCCCT	CAATCC	ATGTAG	GG	1440
1441	ACATCT	GAGTAT	GCCCTC	TTTCTA	TGAAAT	GTCAAT	TCAATC	CCAGCT	TTTCTC	ACCACCG		1500
1501	TTCCCC	TTTGAT	TTCTCA	ATTGTC	TTTTTG	CCCTTT	AGCTCC	CACCTA	TACATC	TCTCAT		1560
1561	GCTCAG	AGAAA	ACAAGT	TCCTTA	GAGGTG	TATTC	TTTAT	TCTCCA	AGAA	TCTGTC	TGA	1620
1621	AACTTG	TACAGT	AGTTCC	CTGTCC	CACTA	TAAAGT	GGTTAT	TAAAGT	ACATTA	GAGCA		1680
1681	GAATGT	GCACTT	CATCAC	CAGGTT	CTAGCT	CTGGCA	AAGAGT	GCTGTC	TACAGC	CAAGAT		1740
1741	TTTTTG	CTTTTA	GAATTT	TATTA	CTACTA	CTCTTG	GGTTCA	TCCATC	TACAA	CACTGAT		1800

FIG. 10E

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1801	TAAGGCCCTTGGGCAACCAATTGATCAGATTACTAAAGGACTTGGGAAAAGCAAAA	1860
1861	AGTCCCATTTGTACTGGTACTGAGGATTAGAAGCAATTGAAATACAAGCCTGTACCAAGC	1920
1921	AAGCAGCCTGGCCCCACACAGGTATTAGCAAATAATGTGGTAACCAAGTTTTAGGCCTTG	1980
1981	GSCYCTAGGTTCCCTGTTTTTTTTCGTTTGGTTTCCGTTTTCGTTTTTTTGCAACAGGT	2040
2041	TATTCTTATCTCACTGGCTTTCACCTGATCATGTTTAGACCTTCTGTAGAAGAAATAATA	2100
2101	TCCAGACAGGGGATGATTGGCTTCAGCAGGCTGCAGGTGTTCAAAGTTGCCATGTGGC	2160
2161	TGGCAGTGGTTCAAGCCCACATTTGACACTGCTGCTCTAGAGGAAAGATAATGATGGTAA	2220

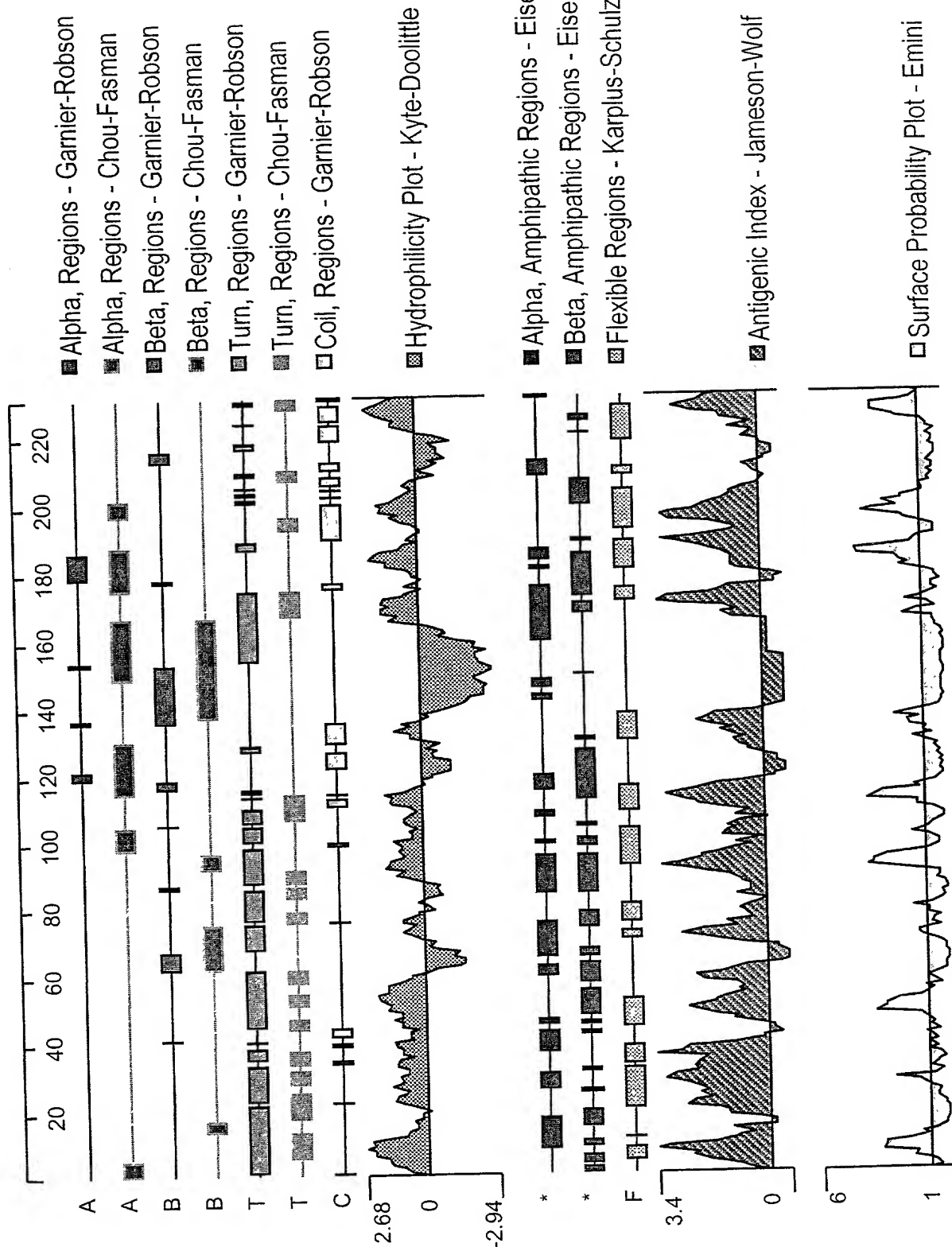
FIG. 10F

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2221	CACAGTAAATAATAATAACAAAATATGATAAAGTGAAGAGTAGATTCTTTCA	2280
2281	GTGTGCTTGCTCCATGGCATGAATGCTATGTGGACAGCCCAAGCCATACCCAGAAATCACC	2340
2341	TTAATTCCAACTTTTGGAGGTTTCAGCAATTGGAGGTGGCAATTGGCTTTGCATTTTAAAG	2400
2401	TATTTGGGTAAAGTGAAGTGAAGGATTTTCGTCCTTTATAAATTTCTGTTTGGCCATGGC	2460
2461	AAATACCATAGTTGAGTATTTTGCTTCAGGAGAGTTCTTTTACAGTTTACTTTTCAATG	2520
2521	CTGAGGCATATTTCTTTGAGCACCTGTGCTTTTATGTGCTCTTTCTACAAGGGTTATTGG	2580
2581	TCAGTGAAGAACAAAGTACACTTGATAAAAAACATTTTCAACATACATTGAGCCTAACA	2640
2641	GCAGTTAAGTTGTCTCTAATGAAGTACCAAAAAAAAATGTAGTTTGTGTTGTAAGG	2700

FIG. 10G

FIG. 10H



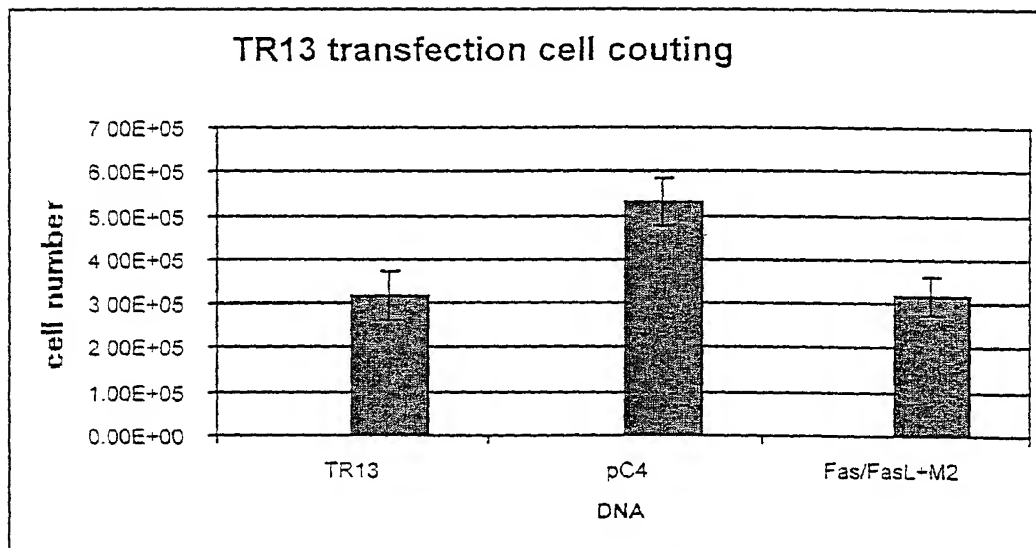


FIG. 12